For GOI from the core + AG replacing NN:

TACTTCCAATCCATGGCGGTTCGTGAACTGCCGGGTGCGTGGAACTTCCGCGACGTGGCTGACACCGCGACCGCGCTGCGTCCGGGTCGTCTGTTCCGTAGCTCTGAACTGTCTCGTCTCGATGATGCCGGTCGTGCCACCCTGCGCCGTCTGGGTATCACCGACGTTGCCGATCTCCGCTCTTCCCGTGAAGTTGCTCGTCGTGGTCCAGGTCGTGTTCCAGATGGTATCGACGTTCACCTGCTGCCGTTTCCTGATCTCGCGGACGATGACGCGGATGACTCTGCGCCTCACGAAACCGCATTCAAACGTCTGCTGACCAACGACGGCTCTAATGGCGAATCTGGTGAATCTTCTCAGTCTATCAATGATGCAGCCACTCGTTACATGACCGACGAATATCGTCAATTCCCGACCCGTAATGGTGCGCAGCGTGCCCTGCATCGTGTTGTAACCCTCCTGGCCGCTGGCCGTCCGGTTCTGACCCACTGCTTTGCGGGTAAAGACCGTACCGGCTTCGTTGTTGCACTGGTTCTGGAAGCGGTTGGTCTGGATCGTGACGTAATTGTGGCGGACTACCTCCGTTCTAACGACAGCGTTCCGCAACTGCGTGCGCGTATCTCTGAAATGATCCAGCAGCGTTTCGACACCGAACTGGCACCGGAGGTTGTTACCTTCACCAAAGCGCGTCTGTCTGACGGCGTTCTCGGTGTTCGTGCGGAATACCTGGCAGCGGCTCGTCAAACCATCGACGAAACTTACGGTTCTCTGGGTGGTTACCTGCGTGATGCGGGCATCTCTCAGGCGACCGTTAACCGTATGCGTGGTGTTCTCCTGGGTTAACAGTAAAGGTGGATA

Reverse GOI from the core:

TATCCACCTTTACTGTTAACCCAGGAGAACACCACGCATACGGTTAACGGTCGCCTGAGAGATGCCCGCATCACGCAGGTAACCACCCAGAGAACCGTAAGTTTCGTCGATGGTTTGACGAGCCGCTGCCAGGTATTCCGCACGAACACCGAGAACGCCGTCAGACAGACGCGCTTTGGTGAAGGTAACAACCTCCGGTGCCAGTTCGGTGTCGAAACGCTGCTGGATCATTTCAGAGATACGCGCACGCAGTTGCGGAACGCTGTCGTTAGAACGGAGGTAGTCCGCCACAATTACGTCACGATCCAGACCAACCGCTTCCAGAACCAGTGCAACAACGAAGCCGGTACGGTCTTTACCCGCAAAGCAGTGGGTCAGAACCGGACGGCCAGCGGCCAGGAGGGTTACAACACGATGCAGGGCACGCTGCGCACCATTACGGGTCGGGAATTGACGATATTCGTCGGTCATGTAACGAGTGGCTGCATCATTGATAGACTGAGAAGATTCACCAGATTCGCCATTAGAGCCGTCGTTGGTCAGCAGACGTTTGAATGCGGTTTCGTGAGGCGCAGAGTCATCCGCGTCATCGTCCGCGAGATCAGGAAACGGCAGCAGGTGAACGTCGATACCATCTGGAACACGACCTGGACCACGACGAGCAACTTCACGGGAAGAGCGGAGATCGGCAACGTCGGTGATACCCAGACGGCGCANGGTGGCACGACCGGCATCATCGAGACGAGACAGTTCAGAGCTACGGAACAGACGACCCGGACGCAGCGCGGTCGCGGTGTCAGCCACGTCGCGGAAGTTCCACGCACCCGGCAGTTCACGAACCGCCATGGNTTGGAAGTA

Query: For sequence from the core inputted

Sbjct: Rev sequence from the core inputted

>lcl|37593

Length=858

Score = 1570 bits (850), Expect = 0.0

Identities = 854/858 (99%), Gaps = 0/858 (0%)

Strand=Plus/Minus

Query 1 TACTTCCAATCCATGGCGGTTCGTGAACTGCCGGGTGCGTGGAACTTCCGCGACGTGGCT 60

||||||||| ||||||||||||||||||||||||||||||||||||||||||||||||||

Sbjct 858 TACTTCCAANCCATGGCGGTTCGTGAACTGCCGGGTGCGTGGAACTTCCGCGACGTGGCT 799

Query 61 GACACCGCGACCGCGCTGCGTCCGGGTCGTCTGTTCCGTAGCTCTGAACTGTCTCGTCTC 120

||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||

Sbjct 798 GACACCGCGACCGCGCTGCGTCCGGGTCGTCTGTTCCGTAGCTCTGAACTGTCTCGTCTC 739

Query 121 GATGATGCCGGTCGTGCCACCCTGCGCCGTCTGGGTATCACCGACGTTGCCGATCTCCGC 180

||||||||||||||||||||| ||||||||||||||||||||||||||||||||||||||

Sbjct 738 GATGATGCCGGTCGTGCCACCNTGCGCCGTCTGGGTATCACCGACGTTGCCGATCTCCGC 679

Query 181 TCTTCCCGTGAAGTTGCTCGTCGTGGTCCAGGTCGTGTTCCAGATGGTATCGACGTTCAC 240

||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||

Sbjct 678 TCTTCCCGTGAAGTTGCTCGTCGTGGTCCAGGTCGTGTTCCAGATGGTATCGACGTTCAC 619

Query 241 CTGCTGCCGTTTCCTGATCTCGCGGACGATGACGCGGATGACTCTGCGCCTCACGAAACC 300

||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||

Sbjct 618 CTGCTGCCGTTTCCTGATCTCGCGGACGATGACGCGGATGACTCTGCGCCTCACGAAACC 559

Query 301 GCATTCAAACGTCTGCTGACCAACGACGGCTCTAATGGCGAATCTGGTGAATCTTCTCAG 360

||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||

Sbjct 558 GCATTCAAACGTCTGCTGACCAACGACGGCTCTAATGGCGAATCTGGTGAATCTTCTCAG 499

Query 361 TCTATCAATGATGCAGCCACTCGTTACATGACCGACGAATATCGTCAATTCCCGACCCGT 420

||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||

Sbjct 498 TCTATCAATGATGCAGCCACTCGTTACATGACCGACGAATATCGTCAATTCCCGACCCGT 439

Query 421 AATGGTGCGCAGCGTGCCCTGCATCGTGTTGTAACCCTCCTGGCCGCTGGCCGTCCGGTT 480

||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||

Sbjct 438 AATGGTGCGCAGCGTGCCCTGCATCGTGTTGTAACCCTCCTGGCCGCTGGCCGTCCGGTT 379

Query 481 CTGACCCACTGCTTTGCGGGTAAAGACCGTACCGGCTTCGTTGTTGCACTGGTTCTGGAA 540

||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||

Sbjct 378 CTGACCCACTGCTTTGCGGGTAAAGACCGTACCGGCTTCGTTGTTGCACTGGTTCTGGAA 319

Query 541 GCGGTTGGTCTGGATCGTGACGTAATTGTGGCGGACTACCTCCGTTCTAACGACAGCGTT 600

||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||

Sbjct 318 GCGGTTGGTCTGGATCGTGACGTAATTGTGGCGGACTACCTCCGTTCTAACGACAGCGTT 259

Query 601 CCGCAACTGCGTGCGCGTATCTCTGAAATGATCCAGCAGCGTTTCGACACCGAACTGGCA 660

||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||

Sbjct 258 CCGCAACTGCGTGCGCGTATCTCTGAAATGATCCAGCAGCGTTTCGACACCGAACTGGCA 199

Query 661 CCGGAGGTTGTTACCTTCACCAAAGCGCGTCTGTCTGACGGCGTTCTCGGTGTTCGTGCG 720

||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||

Sbjct 198 CCGGAGGTTGTTACCTTCACCAAAGCGCGTCTGTCTGACGGCGTTCTCGGTGTTCGTGCG 139

Query 721 GAATACCTGGCAGCGGCTCGTCAAACCATCGACGAAACTTACGGTTCTCTGGGTGGTTAC 780

||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||

Sbjct 138 GAATACCTGGCAGCGGCTCGTCAAACCATCGACGAAACTTACGGTTCTCTGGGTGGTTAC 79

Query 781 CTGCGTGATGCGGGCATCTCTCNNGCGACCGTTAACCGTATGCGTGGTGTTCTCCTGGGT 840

|||||||||||||||||||||| ||||||||||||||||||||||||||||||||||||

Sbjct 78 CTGCGTGATGCGGGCATCTCTCAGGCGACCGTTAACCGTATGCGTGGTGTTCTCCTGGGT 19

Query 841 TAACAGTAAAGGTGGATA 858

||||||||||||||||||

Sbjct 18 TAACAGTAAAGGTGGATA 1

For GOI from the core + AG blasted with GOI:

>lcl|54427

Length=858

Score = 1585 bits (858), Expect = 0.0

Identities = 858/858 (100%), Gaps = 0/858 (0%)

Strand=Plus/Plus

Query 1 TACTTCCAATCCATGGCGGTTCGTGAACTGCCGGGTGCGTGGAACTTCCGCGACGTGGCT 60

||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||

Sbjct 1 TACTTCCAATCCATGGCGGTTCGTGAACTGCCGGGTGCGTGGAACTTCCGCGACGTGGCT 60

Query 61 GACACCGCGACCGCGCTGCGTCCGGGTCGTCTGTTCCGTAGCTCTGAACTGTCTCGTCTC 120

||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||

Sbjct 61 GACACCGCGACCGCGCTGCGTCCGGGTCGTCTGTTCCGTAGCTCTGAACTGTCTCGTCTC 120

Query 121 GATGATGCCGGTCGTGCCACCCTGCGCCGTCTGGGTATCACCGACGTTGCCGATCTCCGC 180

||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||

Sbjct 121 GATGATGCCGGTCGTGCCACCCTGCGCCGTCTGGGTATCACCGACGTTGCCGATCTCCGC 180

Query 181 TCTTCCCGTGAAGTTGCTCGTCGTGGTCCAGGTCGTGTTCCAGATGGTATCGACGTTCAC 240

||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||

Sbjct 181 TCTTCCCGTGAAGTTGCTCGTCGTGGTCCAGGTCGTGTTCCAGATGGTATCGACGTTCAC 240

Query 241 CTGCTGCCGTTTCCTGATCTCGCGGACGATGACGCGGATGACTCTGCGCCTCACGAAACC 300

||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||

Sbjct 241 CTGCTGCCGTTTCCTGATCTCGCGGACGATGACGCGGATGACTCTGCGCCTCACGAAACC 300

Query 301 GCATTCAAACGTCTGCTGACCAACGACGGCTCTAATGGCGAATCTGGTGAATCTTCTCAG 360

||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||

Sbjct 301 GCATTCAAACGTCTGCTGACCAACGACGGCTCTAATGGCGAATCTGGTGAATCTTCTCAG 360

Query 361 TCTATCAATGATGCAGCCACTCGTTACATGACCGACGAATATCGTCAATTCCCGACCCGT 420

||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||

Sbjct 361 TCTATCAATGATGCAGCCACTCGTTACATGACCGACGAATATCGTCAATTCCCGACCCGT 420

Query 421 AATGGTGCGCAGCGTGCCCTGCATCGTGTTGTAACCCTCCTGGCCGCTGGCCGTCCGGTT 480

||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||

Sbjct 421 AATGGTGCGCAGCGTGCCCTGCATCGTGTTGTAACCCTCCTGGCCGCTGGCCGTCCGGTT 480

Query 481 CTGACCCACTGCTTTGCGGGTAAAGACCGTACCGGCTTCGTTGTTGCACTGGTTCTGGAA 540

||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||

Sbjct 481 CTGACCCACTGCTTTGCGGGTAAAGACCGTACCGGCTTCGTTGTTGCACTGGTTCTGGAA 540

Query 541 GCGGTTGGTCTGGATCGTGACGTAATTGTGGCGGACTACCTCCGTTCTAACGACAGCGTT 600

||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||

Sbjct 541 GCGGTTGGTCTGGATCGTGACGTAATTGTGGCGGACTACCTCCGTTCTAACGACAGCGTT 600

Query 601 CCGCAACTGCGTGCGCGTATCTCTGAAATGATCCAGCAGCGTTTCGACACCGAACTGGCA 660

||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||

Sbjct 601 CCGCAACTGCGTGCGCGTATCTCTGAAATGATCCAGCAGCGTTTCGACACCGAACTGGCA 660

Query 661 CCGGAGGTTGTTACCTTCACCAAAGCGCGTCTGTCTGACGGCGTTCTCGGTGTTCGTGCG 720

||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||

Sbjct 661 CCGGAGGTTGTTACCTTCACCAAAGCGCGTCTGTCTGACGGCGTTCTCGGTGTTCGTGCG 720

Query 721 GAATACCTGGCAGCGGCTCGTCAAACCATCGACGAAACTTACGGTTCTCTGGGTGGTTAC 780

||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||

Sbjct 721 GAATACCTGGCAGCGGCTCGTCAAACCATCGACGAAACTTACGGTTCTCTGGGTGGTTAC 780

Query 781 CTGCGTGATGCGGGCATCTCTCAGGCGACCGTTAACCGTATGCGTGGTGTTCTCCTGGGT 840

||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||

Sbjct 781 CTGCGTGATGCGGGCATCTCTCAGGCGACCGTTAACCGTATGCGTGGTGTTCTCCTGGGT 840

Query 841 TAACAGTAAAGGTGGATA 858

||||||||||||||||||

Sbjct 841 TAACAGTAAAGGTGGATA 858